

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/677,877A  
Source: FWO  
Date Processed by STIC: 5/23/05

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 05/23/2005

PATENT APPLICATION: US/10/677,877A

TIME: 10:08:07

Input Set : A:\GHtrimer.txt

Output Set: N:\CRF4\05232005\J677877A.raw

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4 <110> APPLICANT: Liang, Peng; GenHunter Corporation
6 <120> TITLE OF INVENTION: Methods and composition for producing secreted trimeric
7   receptor analogs and biologically active fusion proteins
9 <130> FILE REFERENCE: 03-052-PL
11 <140> CURRENT APPLICATION NUMBER: 10/677,877A
12 <141> CURRENT FILING DATE: 2003-10-02
14 <160> NUMBER OF SEQ ID NOS: 16
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 963
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (12)...(947)
25 <400> SEQUENCE: 1
26 aagcttacgt aagatctaac ggtctccctg gccccattgg gccccctggt cctcgcggtc   60
28 gcaactggta tgctggctct gttggtcccc ccggccctcc tggacctcct ggtccccctg  120
30 gtcctcccag cgctgggttc gacttcagct tcctgcccc gccacctcaa gagaaggctc   180
32 acgatgggtg ccgctactac cgggctgatg atgccaatgt ggttcgtgac cgtgacctcg   240
34 aggtggacac caccctcaag agcctgagcc agcagatcga gaacatccgg agcccagagg   300
36 gaagccgcaa gaaccccggc cgcacctgcc gtgacctcaa gatgtgccac tctgactgga   360
38 agagtggaga gtactggatt gaccccaacc aaggctgcaa cctggatgcc atcaaagtct   420
40 tctgcaacat ggagactggt gagacctgcg tgtacccac tcagcccagt gtggcccaga   480
42 agaactggta catcagcaag aaccccaagg acaagaggca tgtctggttc ggcgagagca   540
44 tgaccgatgg attccagttc gagtatggcg gccagggtc cgacctgcc gatgtggcca   600
46 tccagctgac ctctctgcgc ctgatgtcca ccgaggcctc ccagaacatc acctaccact   660
48 gcaagaacag cgtggcctac atggaccagc agactggcaa cctcaagaag gccctgctcc   720
50 tcaagggtc caacgagatc gagatccgcg ccgagggcaa cagccgcttc acctacagcg   780
52 tcaactgtcg tggctgcacg agtcacaccg gagcctgggg caagacagtg attgaataga   840
54 aaaccaccaa gtcctccgcg ctgcccatca tcgatgtggc ccccttgga gttggtgccc   900
56 cagaccagga attcggcttc gacgttggcc ctgtctgctt cctgtaaact ccctccatct   960
58 aga
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 311
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 2
67 Arg Ser Asn Gly Leu Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly
68      5              10              15
70 Arg Thr Gly Asp Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly Pro
71      20              25              30
73 Pro Gly Pro Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe Leu
74      35              40              45

```

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76 Pro Gln Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr Arg
77      50                      55                      60
79 Ala Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp Thr
80 65                      70                      75                      80
82 Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro Glu
83                      85                      90                      95
85 Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met Cys
86                      100                     105                     110
88 His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln Gly
89                      115                     120                     125
91 Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly Glu
92                      130                     135                     140
94 Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp Tyr
95 145                     150                     155                     160
97 Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu Ser
98                      165                     170                     175
100 Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp Pro
101                      180                     185                     190
103 Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr Glu
104                      195                     200                     205
106 Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr Met
107                      210                     215                     220
109 Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Lys Gly Ser
110 225                     230                     235                     240
112 Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr Ser
113                      245                     250                     255
115 Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys Thr
116                      260                     265                     270
118 Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile Asp
119                      275                     280                     285
121 Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe Asp
122                      290                     295                     300
124 Val Gly Pro Val Cys Phe Leu
125 305                      310
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 771
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (12)...(755)
138 <400> SEQUENCE: 3
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141 ccctcaagag cctgagccag cagatcgaga acatccggag cccagaggga agccgcaaga 120
143 accccgcccg cacctgccgt gacctcaaga tgtgccactc tgactggaag agtggagagt 180
145 actggattga cccaaccaa ggctgcaacc tggatgccat caaagtcttc tgcaacatgg 240
147 agactggtga gacctgcgtg taccctcactc agcccagtggt ggcccagaag aactggtaca 300
149 tcagcaagaa cccaaggac aagaggcatg tctggttcgg cgagagcatg accgatggat 360
151 tccagttcga gtatggcggc cagggtccg accctgccga tgtggccatc cagctgacct 420

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153 tcctgcgcct gatgtccacc gaggcctccc agaacatcac ctaccactgc aagaacagcg 480
155 tggcctacat ggaccagcag actggcaacc tcaagaaggc cctgctcctc aagggctcca 540
157 acgagatcga gatccgcgcc gagggcaaca gccgcttcac ctacagcgtc actgtcgatg 600
159 gctgcacgag tcacaccgga gcctggggca agacagtgat tgaatacaaa accaccaagt 660
161 cctcccgcct gcccatcatc gatgtggccc ccttgacgtg tggtgcccca gaccaggaat 720
163 tcggcttcga cgttggccct gtctgcttcc tgtaaactcc ctccatctag a 771

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166 &lt;210&gt; SEQ ID NO: 4

167 &lt;211&gt; LENGTH: 247

168 &lt;212&gt; TYPE: PRT

169 &lt;213&gt; ORGANISM: Homo sapiens

171 &lt;400&gt; SEQUENCE: 4

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172 Arg Ser Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp Thr
173 1 5 10 15
175 Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro Glu
176 20 25 30
178 Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met Cys
179 35 40 45
181 His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln Gly
182 50 55 60
184 Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly Glu
185 65 70 75 80
187 Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp Tyr
188 85 90 95
190 Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu Ser
191 100 105 110
193 Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp Pro
194 115 120 125
196 Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr Glu
197 130 135 140
199 Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr Met
200 145 150 155 160
202 Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly Ser
203 165 170 175
205 Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr Ser
206 180 185 190
208 Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys Thr
209 195 200 205
211 Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile Asp
212 210 215 220
214 Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe Asp
215 225 230 235 240
217 Val Gly Pro Val Cys Phe Leu
218 245

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220 &lt;210&gt; SEQ ID NO: 5

221 &lt;211&gt; LENGTH: 2487

222 &lt;212&gt; TYPE: DNA

223 &lt;213&gt; ORGANISM: Homo sapiens

225 &lt;220&gt; FEATURE:

226 &lt;221&gt; NAME/KEY: CDS

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227 &lt;222&gt; LOCATION: (12)...(2471)

229 &lt;400&gt; SEQUENCE: 5

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230 aagcttcctg catgctgctg ctgctgctgc tgctgggctt gaggetacag ctctccctgg 60
232 gcatcatccc agttgaggag gagaacccgg acttctggaa ccgcgaggca gccgaggccc 120
234 tgggtgccgc caagaagctg cagcctgcac agacagccgc caagaacctc atcatcttcc 180
236 tgggcgatgg gatgggggtg tctacgggtg cagctgccag gatcctaaaa gggcagaaga 240
238 aggacaaact ggggcctgag atacccttgg ccatggaccg cttcccatat gtggctctgt 300
240 ccaagacata caatgtagac aaacatgtgc cagacagtgg agccacagcc acggcctacc 360
242 tgtgcggggg caagggcaac ttccagacca ttggcttgag tgcagccgcc cgctttaacc 420
244 agtgcaaacac gacacgcggc aacgaggtca tctccgtgat gaatcggggc aagaaagcag 480
246 ggaagtcagt gggagtggta accaccacac gagtgcagca cgcctcgcca gccggcacct 540
248 acgcccacac ggtgaaccgc aactggtact cggacgccga cgtgcctgcc tcggcccgcc 600
250 aggaggggtg ccaggacatc gctacgcagc tcatctccaa catggacatt gacgtgatcc 660
252 taggtggagg ccgaaagtac atgtttccca tgggaacccc agaccctgag taccagatg 720
254 actacagcca aggtgggacc aggtggagc ggaagaatct ggtgcaggaa tggctggcga 780
256 agcgccaggg tgcccgggat gtgtggaacc gcactgagct catgcaggct tccctggacc 840
258 cgtctgtgac ccatctcatg ggtctctttg agcctggaga catgaaatac gagatccacc 900
260 gagactccac actggacccc tccctgatgg agatgacaga ggctgccctg cgcctgctga 960
262 gcaggaaaccc ccgcggcttc ttctcttctg tggaggggtg tcgcatcgac catggtcatc 1020
264 atgaaagcag ggcttaccgg gcactgactg agacgatcat gttcgacgac gccattgaga 1080
266 gggcgggcca gctcaccagc gaggaggaca cgtgagcct cgtcactgcc gaccactccc 1140
268 acgtcttctc cttcggaggc taccctctgc gaggagctc catcttcggg ctggcccctg 1200
270 gcaaggcccg ggacaggaag gcctacacgg tctctctata cggaaacggg ccaggctatg 1260
272 tgctcaagga cggcgcccg cgggatgta ccgagacga gagcgggagc cccgagtatc 1320
274 ggcagcagtc agcagtggc ctggacgaag agaccacgc aggcgaggac gtggcgggtg 1380
276 tcgcgcgcgg cccgcaggcg caccctggtc acggcgtgca ggagcagacc ttcatagcgc 1440
278 acgtcatggc cttcgcgcgc tgccctggagc cctacaccgc ctgcgacctg gcgccccccg 1500
280 ccggcaccac cgacgcgcgc cacccggtt ccggaagatc taacggtctc cctggcccca 1560
282 ttgggcccc tggtcctgc ggtgcactg gtgatgctgg tctgttggg cccccggcc 1620
284 ctcttgacc tctggtccc cctggtctc ccagcgtgg tttcgacttc agcttctgc 1680
286 cccagccacc tcaagagaag gctcacgat gtggccgcta ctaccgggct gatgatgcca 1740
288 atgtggttcg tgaccgtgac ctcgaggtgg acaccacct caagagcctg agccagcaga 1800
290 tcgagaacat ccggagccca gagggaaagg gcaagaaccc cgcgcgacc tgccgtgacc 1860
292 tcaagatgtg ccaactctgac tggaaagagt gagagtactg gattgacccc aaccaaggct 1920
294 gcaacctgga tgccatcaaa gtcttctgca acatggagac tggtgagacc tgctgttacc 1980
296 ccaactcagc cagtgtggcc cagaagaact ggtacatcag caagaacccc aaggacaaga 2040
298 ggcatgtctg gttcggcgag agcatgaccg atggattcca gttcgagtat ggcggccagg 2100
300 gctccgaccc tgccgatgtg gccatccagc tgaccttctt gcgcctgatg tccaccgagg 2160
302 cctcccagaa catcacctac cactgcaaga acagcgtggc ctacatggac cagcagactg 2220
304 gcaacctcaa gaaggccctg ctctcaagg gctccaacga gatcgagatc cgcgcgagg 2280
306 gcaacagccg cttcacctac agcgtcactg tcgatggctg cagagtcac accggagcct 2340
308 ggggcaagac agtgattgaa taaaaacca ccaagtcctc ccgcctgccc atcatcgatg 2400
310 tggccccctt ggacgttggt gccccagacc aggaattcgg cttcgacgtt ggccctgtct 2460
312 gcttctctga aactccctcc atctaga 2487

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315 &lt;210&gt; SEQ ID NO: 6

316 &lt;211&gt; LENGTH: 819

317 &lt;212&gt; TYPE: PRT

318 &lt;213&gt; ORGANISM: Homo sapiens

320 &lt;400&gt; SEQUENCE: 6

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321 Met Leu Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu
322      5      10      15
324 Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
325      20      25      30
327 Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
328      35      40      45
330 Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
331      50      55      60
333 Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
334      65      70      75      80
336 Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
337      85      90      95
339 Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
340      100     105     110
342 Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
343      115     120     125
345 Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
346      130     135     140
348 Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
349      145     150     155     160
351 Gly Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
352      165     170     175
354 Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
355      180     185     190
357 Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
358      195     200     205
360 Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met
361      210     215     220
363 Phe Pro Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
364      225     230     235     240
366 Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
367      245     250     255
369 Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
370      260     265     270
372 Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
373      275     280     285
375 Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
376      290     295     300
378 Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
379      305     310     315     320
381 Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
382      325     330     335
384 His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
385      340     345     350
387 Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
388      355     360     365
390 Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
391      370     375     380
393 Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 05/23/2005  
PATENT APPLICATION: US/10/677,877A      TIME: 10:08:08

Input Set : A:\GHtrimer.txt  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:7; Line(s) 564  
Seq#:11; Line(s) 961  
Seq#:14; Line(s) 1274  
Seq#:15; Line(s) 1364

VERIFICATION SUMMARY

DATE: 05/23/2005

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